RAW SEQUENCE LISTING

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Application Serial Number: _10/537,557_

Source: _FWP_

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RAW SEQUENCE LISTING   DATE: 04/14/2006
PATENT APPLICATION: US/10/537,557   TIME: 11:28:18

Input Set : **A:\Sequence.txt**
Output Set: **N:\CRF4\04142006\J537557.raw**

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 3 <110> APPLICANT: Jaffray, Ann
 4        Williamson, Anna-Lise
 5        Rybicki, Edward Peter
 7 <120> TITLE OF INVENTION: A Method for the Production of HIV-1 GAG Virus-Like
Particles
 9 <130> FILE REFERENCE: 45669-316582
11 <140> CURRENT APPLICATION NUMBER: US 10/537,557
12 <141> CURRENT FILING DATE: 2005-06-03
14 <150> PRIOR APPLICATION NUMBER: PCT/IB03/005634
15 <151> PRIOR FILING DATE: 2003-12-04
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1549
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1
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29 attaggttaa ggccaggggg aaagaaacat tatatgttaa aacacatagt atgggcgagc    120
31 agggagctgg aaagatttgc acttaaccct ggccttttag aaacatcaga aggatgtaaa    180
33 caaataatga aacagctaca accagctctc cagacaggaa cagaggaact aaatcatta     240
35 tacaacacag tagcaactct ctattgtgta catgaaaaga tagaagtacg agacaccaag    300
37 gaagccttag ataagataga ggaagaacaa aacaaatgtc agcaaaaaac gcagcaggca    360
39 aaagcggctg acgggaaagt cagtcaaaat tatcctatag tgcagaatct ccaagggcaa    420
41 atggtacatc aagccatatc acctagaacc ttgaatgcat gggtaaaagt aatagaagaa    480
43 aaggctttta gcccagaggt aatacccatg tttacagcat tatcagaagg agccacccca    540
45 caagatttaa acaccatgtt aaatacagtg gggggacacc aagcagccat gcaaatgtta    600
47 aaagatacta ttaatgaaga ggctgcagaa tgggatagat tacatccagt ccatgcgggg    660
49 cctattgcac caggccagat gagagaacca aggggaagtg acatagcagg aactactagt    720
51 acccttcagg aacaaatagc atggatgaca agtaacccac ctattccagt gggagacatc    780
53 tataaaagat ggataattct ggggttaaat aaaatagtga gaatgtatag cccggtcagc    840
55 attttggaca taagacaagg gccaaaggaa cccttcgag actatgtaga tcggttcttt    900
57 aaaactttaa gagctgaaca agctacacaa gaagtaaaaa attggatgac agacaccttg    960
59 ttagtccaaa atgcgaaccc agattgtaag accattttga gagcattagg accaggggct   1020
61 acattagaag aaatgatgac agcatgtcaa ggggtgggag gacctggcca caaagcaaga   1080
63 gtattggctg aggcaatgag tcaaacaaac agtggaaaca taatgatgca gagaagcaat   1140
65 tttaaaggcc ctagaagaat tgttaaatgt tttaactgtg gcaaggaagg gcacatagcc   1200
67 agaaattgca gagccctag gaaaaaaggc tgttggaaat gtggaaaaga aggacaccaa   1260
69 atgaaagact gcactgagag gcaggctaat tttttaggga aaatttggcc ttcccacaag   1320
71 gggaggccag ggaatttcct tcagaacaga ccagagccaa cagccccacc agcagagagc   1380
73 ttcaggttcg aagagacaac ccccgctccg aaacaggagc cgatagaaag gaacccctta   1440
75 acttccctca aatcactctt tggcagcgac cccttgtctc aataaaagta gggggccaga   1500
77 caagggaggc tctcttagac acaggagcag atgatacagt attgtcgac              1549
80 <210> SEQ ID NO: 2
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 82 <212> TYPE: DNA
 83 <213> ORGANISM: Homo sapiens
 85 <400> SEQUENCE: 2
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 88 ttaaggccag ggggaaagaa acattatatg ttaaaacaca tagtatgggc gagcagggag    120
 90 ctggaaagat ttgcacttaa ccctggcctt ttagaaacat cagaaggatg taaacaaata    180
 92 atgaaacagc tacaaccagc tctccagaca ggaacagagg aacttaaatc attatacaac    240
 94 acagtagcaa ctctctattg tgtacatgaa aagatagaag tacgagacac caaggaagcc    300
 96 ttagataaga tagaggaaga acaaaacaaa tgtcagcaaa aaacgcagca ggcaaaagcg    360
 98 gctgacggga aagtcagtca aaattatcct atagtgcaga atctccaagg gcaaatggta    420
100 catcaagcca tatcacctag aaccttgaat gcatgggtaa aagtaataga agaaaaggct    480
102 tttagcccag aggtaatacc catgtttaca gcattatcag aaggagccac cccacaagat    540
104 ttaaacacca tgttaaatac agtgggggga caccaagcag ccatgcaaat gttaaaagat    600
106 actattaatg aagaggctgc agaatgggat agattacatc cagtccatgc ggggcctatt    660
108 gcaccaggcc agatgagaga accaagggga agtgacatag caggaactac tagtaccctt    720
110 caggaacaaa tagcatggat gacaagtaac ccacctattc cagtgggaga catctataaa    780
112 agatggataa ttctggggtt aaataaaata gtgagaatgt atagcccggt cagcattttg    840
114 gacataagac aagggccaaa ggaacccttt cgagactatg tagatcggtt ctttaaaact    900
116 ttaagagctg aacaagctac acaagaagta aaaaattgga tgacagacac cttgttagtc    960
118 caaaatgcga acccagattg taagaccatt ttgagagcat taggaccagg ggctacatta   1020
120 gaagaaatga tgacagcatg tcaaggggtg ggaggacctg gccacaaagc aagagtattg   1080
122 gctgaggcaa tgagtcaaac aaacagtgga aacataatga tgcagagaag caattttaaa   1140
124 ggccctagaa gaattgttaa atgttttaac tgtggcaagg aagggcacat agccagaaat   1200
126 tgcagagccc ctaggaaaaa aggctgttgg aaatgtggaa agaaggaca ccaaatgaaa   1260
128 gactgcactg agaggcaggc taattttta gggaaaattt ggccttccca caaggggagg   1320
130 ccagggaatt ccttcagaa cagaccagag ccaacagccc caccagcaga gagcttcagg   1380
132 ttcgaagaga caacccccgc tccgaaacag gagccgatag aaagggaacc cttaacttcc   1440
134 ctcaaatcac tctttggcag cgaccccttg tctcaataa                         1479
137 <210> SEQ ID NO: 3
138 <211> LENGTH: 513
139 <212> TYPE: PRT
140 <213> ORGANISM: Homo aspiens
142 <400> SEQUENCE: 3
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148 Lys Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met
149             20                  25                  30
152 Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Leu
153         35                  40                  45
156 Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Met Lys
157     50                  55                  60
160 Gln Leu Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Lys Ser Leu
161 65                  70                  75                  80
164 Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val
165                 85                  90                  95
168 Arg Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys
169             100                 105                 110
172 Cys Gln Gln Lys Thr Gln Gln Ala Lys Ala Ala Asp Gly Lys Val Ser
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173         115                   120                   125
176 Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln
177      130                   135                   140
180 Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu
181 145                   150                   155                   160
184 Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu
185                   165                   170                   175
188 Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly
189                   180                   185                   190
192 His Gln Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala
193              195                   200                   205
196 Ala Glu Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro
197      210                   215                   220
200 Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser
201 225                   230                   235                   240
204 Thr Leu Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro
205                   245                   250                   255
208 Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
209                   260                   265                   270
212 Val Arg Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro
213              275                   280                   285
216 Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg
217      290                   295                   300
220 Ala Glu Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu
221 305                   310                   315                   320
224 Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu
225                   325                   330                   335
228 Gly Pro Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
229              340                   345                   350
232 Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln
233         355                   360                   365
236 Thr Asn Ser Gly Asn Ile Met Met Gln Arg Ser Asn Phe Lys Gly Pro
237      370                   375                   380
240 Arg Arg Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala
241 385                   390                   395                   400
244 Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys
245                   405                   410                   415
248 Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu
249              420                   425                   430
252 Gly Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln
253         435                   440                   445
256 Asn Arg Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu
257      450                   455                   460
260 Glu Thr Thr Pro Ala Pro Lys Gln Glu Pro Ile Glu Arg Glu Pro Leu
261 465                   470                   475                   480
264 Thr Ser Leu Lys Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln Lys Gly
265                   485                   490                   495
268 Ala Arg Gln Gly Arg Leu Ser Thr Gln Glu Gln Met Ile Gln Tyr Cys
269         500                   505                   510
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Input Set : **A:\Sequence.txt**
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276 <210> SEQ ID NO: 4
277 <211> LENGTH: 492
278 <212> TYPE: PRT
279 <213> ORGANISM: Homo sapiens
281 <400> SEQUENCE: 4
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287 Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys
288             20                  25                  30
291 His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Leu Asn Pro
292         35                  40                  45
295 Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Met Lys Gln Leu
296     50                  55                  60
299 Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Lys Ser Leu Tyr Asn
300 65                  70                  75                  80
303 Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp
304                 85                  90                  95
307 Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln
308             100                 105                 110
311 Gln Lys Thr Gln Gln Ala Lys Ala Ala Asp Gly Lys Val Ser Gln Asn
312         115                 120                 125
315 Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile
316     130                 135                 140
319 Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala
320 145                 150                 155                 160
323 Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala
324                 165                 170                 175
327 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
328             180                 185                 190
331 Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu
332         195                 200                 205
335 Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
336     210                 215                 220
339 Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
340 225                 230                 235                 240
343 Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val Gly
344                 245                 250                 255
347 Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
348             260                 265                 270
351 Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
352         275                 280                 285
355 Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu
356     290                 295                 300
359 Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu Val
360 305                 310                 315                 320
363 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro
364                 325      ·          330                 335
367 Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
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368              340              345              350
371 Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Thr Asn
372          355              360              365
375 Ser Gly Asn Ile Met Met Gln Arg Ser Asn Phe Lys Gly Pro Arg Arg
376      370              375              380
379 Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn
380 385              390              395              400
383 Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
384              405              410              415
387 His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
388          420              425              430
391 Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg
392          435              440              445
395 Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr
396      450              455              460
399 Thr Pro Ala Pro Lys Gln Glu Pro Ile Glu Arg Glu Pro Leu Thr Ser
400 465              470              475              480
403 Leu Lys Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln
404          485              490
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VERIFICATION SUMMARY   DATE: 04/14/2006
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